



## SEQUENCE LISTING

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<110> Parales, R.  
Gibson, D.  
Resnick, S.  
Lee, K.

<120> Novel naphthalene dioxygenase and methods for their use

<130> 875.006US2

<140> US 09/843,250  
<141> 2001-04-26

<150> PCT/US99/25079  
<151> 1999-10-26

<150> US 60/105,575  
<151> 1998-10-26

<160> 65

<170> FastSEQ for Windows Version 4.0

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<223> A sequence encoding an NDO mutant.

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Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val		
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Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His		
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325 330 335		
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340 345 350		

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 355 360 365  
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu  
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 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro  
 385 390 395 400  
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<210> 3  
<211> 9841  
<212> DNA  
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<210> 4  
<211> 2515  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> A modified DNA molecule encoding valine at the position corresponding to the F352 amino acid in NDO.

<400> 4	gaattcatca	ggaagacatt	caaataaataa	gggcagcgtc	tgtatggcg	60
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	aagtggattt	aagcagtcgc	tctttctgac	atccttgaag	gtgacgtctt	180
	gtcgaggggca	aggagctggc	gtcttatgaa	gttgaaggcg	aatctacgc	240
	ctgtgcacgc	atgggtccgc	ccgcatgagt	gatggtttac	tgcagggttag	300
	tgccccttgc	atcaaggctg	gtttgacgtt	tgcacaggca	aagccctgtg	360
	acacagaaca	tcaaaacata	tccagtcaag	attgagaacc	tgcgcgtaat	420
	agctaagaat	tttaacagga	ggcaccccg	gcccttagagc	gtatcaccc	480
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<210> 5  
<211> 9706  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> A modified DNA molecule encoding valine at the position corresponding to the F352 amino acid in NDO.

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aggcaaggctt	tggggccgcgc	tgcacgttac	atacagtaat	gaatttgcgtt	agttcacctc	9600
cgccagaccc	atgtacaggg	tggcgttcc	gctgagggttgc	caggaattaa	gtgagctaaa	9660
gcacatttctt	tgcgttcc	attgcgttcc	cagcaaaatgtt	tgcttgc	9706	

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<210> 6
<211> 2294
<212> DNA
<213> Artificial Sequence
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<220>  
<223> A modified DNA molecule encoding valine at the position corresponding to the F352 amino acid in NDO.

<221> misc\_feature  
<222> (186)...(186)  
<223> n = a or t or g or c

<400> 6

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ggtaatnacg	ctaccgacaa	cctgtgcacg	catggttccg	ccgcacatgag	tgatggttat	180
ctcgagggtt	gagaaatcga	atgccccttgc	catcaaggc	ggtttgcacgt	ttgcacaggc	240
aaagccctgt	gcccacccgt	gacacagaac	atcaaaaacat	atccagtc	gattgagaac	300
ctgcgcgtt	tgattgattt	gagctaagaaa	ttttaacagg	aggcaccccg	ggcccttagag	360
cgttaatcacc	cccattccat	cttttttagg	tgaaaaacat	aattacaata	ataaaaatctt	420
ggttaagtgaa	tttggtctga	gccccaaagca	cctgattcat	ggcgatgaag	aacttttcca	480
acatgaactg	aaaaccattt	ttgcgcggaa	ctggctttt	ctcactcatg	atagcctgat	540
tcctggcccc	ggcgaactatg	ttaccgcaaa	aatggggatt	gacgagggtca	tcgtctcccg	600
gcagaacgac	ggttcgattt	gtgttttctt	gaacgtttgc	cgccatcg	gcaagacgct	660
ggtgagcgtt	gaagccggca	atgcacaaagg	ttttgtttgc	agctatc	gctggggctt	720
cggctccaac	ggtgaactgc	agagcgttcc	atttggggaaa	gatctgtac	gcgagtcgct	780
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ctacttcaca	tccgctccaa	cgtcatt	caccggc	gacgtgg	tgacaaagag	2220
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						2294

<210> 7  
<211> 4355  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> A modified DNA molecule encoding valine at the position corresponding to the F352 amino acid in NDO.

<400> 7

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aagccgcgt	accgcgtcc	ccatatgcct	gagtgtgc	gctaagg	ttcgccg	180
tggcttcgag	aataaagcgg	gccaggtgat	tttctgtca	tctcg	ttgggtgg	240
cacatcaacc	tgaccggcga	ttacgtctgg	cgccagagcc	gcagactg	ggtcggg	300
ttccggccgt	tacggcggcc	ctgaaaac	tagtgc	tttttccgt	tttcttatt	360

cggcctgcgt	tgcgacgttc	gatctgacta	gggcgcagcg	gcaacatcg	ctgagtacga	420
tccagcgctt	ggatctgggt	tatttcgtca	accgacaaca	ccagagcg	ttccgggtgg	480
ttcaggtaaa	gccccaccac	attgactacc	tctcgccaaa	atgagggtcg	ttactaattt	540
tgaacgtctt	caagcgatgg	ggtttttaggt	cggaagctgc	ccagacctgc	ccaacacctt	600
acgtcggtac	ccgagcatat	tccggcccgcg	gcccggaaaaaa	acacagaaat	gagcgggtga	660
cccgtatcgcc	tttgatcgat	tctccgcttt	caaaatggc	gggggctgaa	gtcagccaga	720
aatacatgac	tacttcagac	gattcgca	attcacgctg	gtgataaaaca	aattcaacta	780
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cttaactcaca	attgcggat	cggaaatccca	gaaaccgacg	aaatcg	ccacccggcg	1140
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gaaggtacaa	gcatcaagtt	gagcggggcca	cttggta	tttgc	tcagaaccac	1440
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ccaattccat	ctttttag	tggaa	acatg	tttgc	tttgc	2400
tctggcgtga	cccaa	aa	acttgc	ggc	atgc	2460
agaaccattt	ttgc	gg	cat	tttgc	tttgc	2520
ggc	actat	tttgc	atc	gact	tttgc	2580
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gaagccggca	atgc	cc	tttgc	tttgc	tttgc	2700
ggtgaactgc	agagc	tttgc	tttgc	tttgc	tttgc	2760
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tatcg	cag	tttgc	tttgc	tttgc	tttgc	3300
gtttcaa	at	gg	tttgc	tttgc	tttgc	3360
gtc	aaa	gg	tttgc	tttgc	tttgc	3420
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gacgtatacg	g	gg	tttgc	tttgc	tttgc	3600
agtatcg	gc	gg	tttgc	tttgc	tttgc	3660
ttcgaggat	cct	gg	tttgc	tttgc	tttgc	3720
acgagtcgac	cat	gg	tttgc	tttgc	tttgc	3780
aagagt	ttt	tttgc	tttgc	tttgc	tttgc	3840
tgctgaacc	g	gg	tttgc	tttgc	tttgc	3900
gcgtgggg	ag	gg	tttgc	tttgc	tttgc	3960
gccgttataa	g	ttt	tttgc	tttgc	tttgc	4020
ttcgaatcga	g	ttt	tttgc	tttgc	tttgc	4080

ctcgcttcat caccaatgtc caggccgcaa gggacgtaga tgacgaagag ctacttcaca	4140
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ccgcccggaa agacaaatgg aaacgtggcg aagggtggagt gcgaaaattg gtccagcgat	4260
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<210> 8  
<211> 2176  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> A modified DNA molecule encoding valine at the position corresponding to the F352 amino acid in NDO.

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tcgagggcg agaaatcgaa tgcccccttc atcaaggtcg gtttgcgtt tgtacaggca	180
gagccctctg cgccccctgt acagagaaca tcaaaacata tgcaatgtcaag attgagaacc	240
tgcgcgtaat gattgattta agctgagaat ttttaatagg aggccgcggc gaccatagag	300
cgttaattatc cccattccat ctttttttag gtgaaaacat gaattacaaa aacaaaatct	360
tggtaagtga gtctgggctg accccaaaagc acctgattca tggcgtatgaa gaactttcc	420
agcacgaact gagaaccatt tktgcgcggc actggcttt tctcaactcat gacagcctga	480
ttccttcccc cggcgaactat gttaccgc当地 aaatggggat tgacgaggc当地 atcgtctc当地	540
ggcaaaagcga cggttcgatt cgtgc当地 tgaacgtttt ccggcaccgc ggcaagacac	600
tggtaacgc ggaagccgc aatgctaaag gttcgtttt cagttatcac ggctggggct	660
tcggctccaa cggcgaactg cagagcgtt cattcgaaaa agagctgtac ggccgagtc当地	720
tcaacaaaaa atgtctgggg ttgaaaagaag tcgctc当地 agagagctt catgggttca	780
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gcggatatggg tttgttgc当地 gacggatatt caggcgtc当地 tagcgc当地 ttggttccgg	1140
aattgtatggc attcgccggc gctaaggcagg aaaggctgaa caaagaaaatt ggcatgttc	1200
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gtttc当地 ggtatgtatac ggc当地 acgc当地 tctatc当地 ggatc当地 ctggatc当地 aaatcgcc当地	1560
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<210> 9  
<211> 14462  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> A modified DNA molecule encoding valine at the

position corresponding to the F352 amino acid in  
NDO.

<400> 9		
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tccaaacgatg cgggatcgta cgatgcaggc gctgtggaaa ctggacttg agccgggtgc	180	
cggaaacgcgt gtagatccca actcctatgg atttcggccg cagcgatcca ctggcgatgc	240	
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<213> Artificial Sequence

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<223> A modified DNA molecule encoding valine at the position corresponding to the F352 amino acid in NDO.

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<213> Artificial Sequence

<220>  
<223> A modified DNA molecule encoding valine at the position corresponding to the F352 amino acid in NDO.

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<210> 12  
<211> 4912  
<212> DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; A modified DNA molecule encoding valine at the position corresponding to the F352 amino acid in NDO.

&lt;400&gt; 12

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&lt;210&gt; 13

&lt;211&gt; 6779

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; A modified DNA molecule encoding valine at the position corresponding to the F352 amino acid in NDO.

&lt;400&gt; 13

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cccgaggcgc	ag	tttt	cccaac	cat	gtcaacgct	5820
tgcttggatg	gcgg	ggcattc	gtgattattt	ttaa	aggggc	5880
acacccttgg	ttt	cagt	gag	tttt	gttgc	5940
gtagaccg	ac	gggt	gtat	ccctt	ggccgtt	6000
ggcaatcg	tc	gag	ctgt	ccctt	ttggat	6060
ctggcgcacc	agg	ccatt	ttt	cgtt	ggccc	6120
gcagaagtac	acgg	catt	ggag	cctt	tgc	6180
gccttgg	ta	gtat	ggc	actt	tttgc	6240
gaaggc	aa	gac	gg	ccat	atgc	6300
caccaggc	ct	gg	gg	gg	gttgc	6360
gatgagatc	c	ttt	cc	cc	ccat	6420
atggatg	at	cat	gt	ttt	tttgc	6480
ccg	tt	gt	gg	tttgc	tttgc	6540
catggc	at	gc	gg	tttgc	tttgc	6600
atacaa	ac	gt	gg	tttgc	tttgc	6660
gatcacc	c	gg	gg	tttgc	tttgc	6720
tctgeg	gg	gg	gg	tttgc	tttgc	6779

<210> 14  
<211> 449  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> A polypeptide encoded by SEQ ID NO:3.

<400> 14  
Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln  
1 5 10 15  
Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys  
20 25 30  
Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile  
35 40 45  
Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val  
50 55 60  
Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val  
65 70 75 80  
Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala  
85 90 95  
Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly  
100 105 110  
Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu  
115 120 125  
Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe  
130 135 140  
His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met  
145 150 155 160

Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His  
     165                       170                       175  
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys  
     180                       185                       190  
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His  
     195                       200                       205  
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe  
     210                       215                       220  
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu  
     225                       230                       235                       240  
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly  
     245                       250                       255  
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe  
     260                       265                       270  
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg  
     275                       280                       285  
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn  
     290                       295                       300  
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp  
     305                       310                       315                       320  
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met  
     325                       330                       335  
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val  
     340                       345                       350  
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr  
     355                       360                       365  
 Ala Ser Gln Asn Gly Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu  
     370                       375                       380  
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro  
     385                       390                       395                       400  
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe  
     405                       410                       415  
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe  
     420                       425                       430  
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp  
     435                       440                       445  
 Arg

<210> 15  
 <211> 449  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> A polypeptide encoded by SEQ ID NO:4.

<400> 15  
 Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln  
     1                       5                       10                       15  
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys  
     20                       25                       30  
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile  
     35                       40                       45  
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val  
     50                       55                       60  
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val  
     65                       70                       75                       80  
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala  
     85                       90                       95  
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly  
     100                       105                       110

Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu  
     115                120                125  
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe  
     130                135                140  
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met  
     145                150                155                160  
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His  
     165                170                175  
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys  
     180                185                190  
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His  
     195                200                205  
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe  
     210                215                220  
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu  
     225                230                235                240  
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly  
     245                250                255  
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe  
     260                265                270  
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg  
     275                280                285  
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn  
     290                295                300  
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp  
     305                310                315                320  
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met  
     325                330                335  
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val  
     340                345                350  
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr  
     355                360                365  
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu  
     370                375                380  
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro  
     385                390                395                400  
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe  
     405                410                415  
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe  
     420                425                430  
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp  
     435                440                445  
**Arg**

<210> 16  
 <211> 449  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> A polypeptide encoded by SEQ ID NO:5.

<400> 16  
 Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln  
     1                5                10                15  
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys  
     20                25                30  
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile  
     35                40                45  
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val  
     50                55                60

Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val  
 65 70 75 80  
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala  
 85 90 95  
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly  
 100 105 110  
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu  
 115 120 125  
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe  
 130 135 140  
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met  
 145 150 155 160  
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His  
 165 170 175  
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys  
 180 185 190  
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His  
 195 200 205  
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe  
 210 215 220  
 Cys Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu  
 225 230 235 240  
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly  
 245 250 255  
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe  
 260 265 270  
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg  
 275 280 285  
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn  
 290 295 300  
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp  
 305 310 315 320  
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met  
 325 330 335  
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val  
 340 345 350  
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr  
 355 360 365  
 Ala Ser Gln Asn Gly Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu  
 370 375 380  
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro  
 385 390 395 400  
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe  
 405 410 415  
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe  
 420 425 430  
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp  
 435 440 445  
 Arg

<210> 17  
<211> 449  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> A polypeptide encoded by SEQ ID NO:6.

<400> 17  
Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Phe Gly Leu Ser Gln  
 1 5 10 15

Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys  
     20                       25                       30  
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile  
     35                       40                       45  
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val  
     50                       55                       60  
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val  
     65                       70                       75                       80  
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala  
     85                       90                       95  
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly  
     100                       105                       110  
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu  
     115                       120                       125  
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe  
     130                       135                       140  
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met  
     145                       150                       155                       160  
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His  
     165                       170                       175  
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys  
     180                       185                       190  
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His  
     195                       200                       205  
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe  
     210                       215                       220  
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu  
     225                       230                       235                       240  
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly  
     245                       250                       255  
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe  
     260                       265                       270  
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg  
     275                       280                       285  
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn  
     290                       295                       300  
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp  
     305                       310                       315                       320  
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met  
     325                       330                       335  
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val  
     340                       345                       350  
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr  
     355                       360                       365  
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu  
     370                       375                       380  
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro  
     385                       390                       395                       400  
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe  
     405                       410                       415  
 Tyr Arg Ala Tyr Arg Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe  
     420                       425                       430  
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp  
     435                       440                       445  
 Arg

<210> 18  
 <211> 449  
 <212> PRT  
 <213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; A polypeptide encoded by SEQ ID NO:7.

&lt;400&gt; 18

Met Asn Tyr Lys Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Thr Gln  
 1 5 10 15  
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Arg  
 20 25 30  
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile  
 35 40 45  
 Pro Ser Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val  
 50 55 60  
 Ile Val Ser Arg Gln Ser Asp Gly Ser Ile Arg Ala Phe Leu Asn Val  
 65 70 75 80  
 Cys Arg His Arg Gly Lys Thr Leu Val Asn Ala Glu Ala Gly Asn Ala  
 85 90 95  
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly  
 100 105 110  
 Glu Leu Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Glu Ser Leu  
 115 120 125  
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe  
 130 135 140  
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met  
 145 150 155 160  
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Ile Phe Lys His  
 165 170 175  
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys  
 180 185 190  
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His  
 195 200 205  
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe  
 210 215 220  
 Ala Ser Leu Ala Gly Asn Ala Val Leu Pro Pro Glu Gly Ala Gly Leu  
 225 230 235 240  
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly  
 245 250 255  
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe  
 260 265 270  
 Gly Gly Ser Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg  
 275 280 285  
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn  
 290 295 300  
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp  
 305 310 315 320  
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met  
 325 330 335  
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val  
 340 345 350  
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr  
 355 360 365  
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu  
 370 375 380  
 Ser Asn Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Ala Val Tyr Pro  
 385 390 395 400  
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe  
 405 410 415  
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Asn Trp Ala Glu Phe  
 420 425 430  
 Glu Asp Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp  
 435 440 445  
 Arg

<210> 19  
<211> 449  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> A polypeptide encoded by SEQ ID NO:8.

<221> SITE  
<222> (35)...(35)  
<223> Xaa = any amino acid.

<400> 19  
Met Asn Tyr Lys Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Thr Gln  
1 5 10 15  
Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Arg  
20 25 30  
Thr Ile Xaa Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile  
35 40 45  
Pro Ser Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val  
50 55 60  
Ile Val Ser Arg Gln Ser Asp Gly Ser Ile Arg Ala Phe Leu Asn Val  
65 70 75 80  
Cys Arg His Arg Gly Lys Thr Leu Val Asn Ala Glu Ala Gly Asn Ala  
85 90 95  
Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly  
100 105 110  
Glu Leu Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Glu Ser Leu  
115 120 125  
Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe  
130 135 140  
His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Ser Leu Met  
145 150 155 160  
Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Ile Phe Lys His  
165 170 175  
Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys  
180 185 190  
Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His  
195 200 205  
Val Gly Trp Thr His Ala Ser Ser Leu Arg Thr Gly Glu Ser Ile Phe  
210 215 220  
Ser Ser Leu Ala Gly Asn Ala Val Leu Pro Pro Glu Gly Ala Gly Leu  
225 230 235 240  
Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly  
245 250 255  
Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe  
260 265 270  
Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Pro  
275 280 285  
Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn  
290 295 300  
Ser Val Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp  
305 310 315 320  
Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met  
325 330 335  
Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ala Val Gln Arg Thr Val  
340 345 350  
Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr  
355 360 365  
Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Ile  
370 375 380

Ser Asn Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Ala Val Tyr Pro  
 385                   390                   395                   400  
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe  
                   405                   410                   415  
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe  
                   420                   425                   430  
 Glu Asp Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp  
                   435                   440                   445  
 Arg

<210> 20  
 <211> 449  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> A polypeptide encoded by SEQ ID NO:9.

<400> 20  
 Met Asn Tyr Lys Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Thr Gln  
 1                   5                   10                   15  
 Lys His Leu Ile His Gly Gly Glu Gly Leu Phe Gln His Glu Leu Arg  
 20                   25                   30  
 Ala Val Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile  
 35                   40                   45  
 Pro Ser Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val  
 50                   55                   60  
 Ile Val Ser Arg Gln Ser Asp Gly Ser Ile Arg Ala Phe Leu Asn Val  
 65                   70                   75                   80  
 Cys Arg His Arg Gly Lys Thr Leu Val Asn Ala Glu Ala Gly Asn Ala  
 85                   90                   95  
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly  
 100                  105                  110  
 Glu Leu Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Glu Ser Leu  
 115                  120                  125  
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe  
 130                  135                  140  
 His Gly Phe Ile Tyr Ala Cys Ile Asp Gln Glu Ala Pro Ser Leu Met  
 145                  150                  155                  160  
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Ile Phe Lys His  
 165                  170                  175  
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys  
 180                  185                  190  
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His  
 195                  200                  205  
 Val Gly Trp Thr His Ala Ser Ser Leu Cys Thr Gly Glu Ser Ile Phe  
 210                  215                  220  
 Ser Ser Leu Ala Gly Asn Ala Val Leu Pro Pro Glu Gly Ala Gly Leu  
 225                  230                  235                  240  
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly  
 245                  250                  255  
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe  
 260                  265                  270  
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg  
 275                  280                  285  
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn  
 290                  295                  300  
 Ser Val Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp  
 305                  310                  315                  320  
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met  
 325                  330                  335

Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ala Val Gln Arg Thr Val  
     340                 345                 350  
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr  
     355                 360                 365  
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Ile  
     370                 375                 380  
 Ser Asn Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Ala Val Tyr Pro  
     385                 390                 395                 400  
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe  
     405                 410                 415  
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe  
     420                 425                 430  
 Glu Asp Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp  
     435                 440                 445  
 Arg

<210> 21  
 <211> 449  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> A polypeptide encoded by SEQ ID NO:10.

<400> 21  
 Met Asn Tyr Lys Asn Lys Asn Leu Val Ser Glu Ser Gly Leu Thr Gln  
     1                 5                 10                 15  
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln Arg Glu Leu Glu  
     20                 25                 30  
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile  
     35                 40                 45  
 Pro Ser Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Val Asp Glu Val  
     50                 55                 60  
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val  
     65                 70                 75                 80  
 Cys Arg His Arg Gly Lys Thr Leu Val His Ala Glu Ala Gly Asn Ala  
     85                 90                 95  
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ala Asn Gly  
     100                 105                 110  
 Glu Leu Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Glu Ala Leu  
     115                 120                 125  
 Asp Lys Lys Cys Met Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe  
     130                 135                 140  
 His Gly Phe Ile Tyr Gly Cys Phe Asp Glu Glu Ala Pro Ser Leu Lys  
     145                 150                 155                 160  
 Asp Tyr Met Gly Asp Ala Gly Trp Tyr Leu Glu Pro Met Phe Lys His  
     165                 170                 175  
 Ser Gly Gly Leu Glu Leu Ile Gly Pro Pro Gly Lys Val Ile Ile Lys  
     180                 185                 190  
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Thr Gly Asp Ala Tyr His  
     195                 200                 205  
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Gln Ser Val Phe  
     210                 215                 220  
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu  
     225                 230                 235                 240  
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly  
     245                 250                 255  
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe  
     260                 265                 270  
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Glu Val Arg  
     275                 280                 285

Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn  
 290 295 300  
 Ser Phe Leu Thr Cys Ser Gly Val Phe Lys Val Trp His Pro Ile Asp  
 305 310 315 320  
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Met Val Glu Lys Asp Met  
 325 330 335  
 Pro Glu Asp Leu Lys Arg Arg Leu Val Asp Ala Val Gln Arg Thr Val  
 340 345 350  
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr  
 355 360 365  
 Val Ser Gln Asn Ala Lys Lys Tyr Gln Ser Arg Asp Gly Asp Leu Val  
 370 375 380  
 Ser Asn Leu Gly Phe Gly Gly Asp Val Tyr Gly Asp Glu Val Tyr Pro  
 385 390 395 400  
 Gly Ile Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe  
 405 410 415  
 Tyr Arg Ala Tyr Gly Ala His Ile Ser Ser Ser Trp Ala Glu Phe  
 420 425 430  
 Glu Asp Val Ser Lys Asn Trp His Thr Glu Leu Ala Lys Thr Thr Asp  
 435 440 445  
 Arg

<210> 22  
 <211> 447  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> A polypeptide encoded by SEQ ID NO:11.

<400> 22  
 Met Ile Tyr Glu Asn Leu Val Ser Glu Ala Gly Leu Thr Gln Lys His  
 1 5 10 15  
 Leu Ile His Gly Asp Lys Glu Leu Phe Gln His Glu Leu Lys Thr Ile  
 20 25 30  
 Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile Pro Ser  
 35 40 45  
 Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Val Asp Glu Val Ile Val  
 50 55 60  
 Ser Arg Gln Asn Asp Gly Ser Val Arg Ala Phe Leu Asn Val Cys Arg  
 65 70 75 80  
 His Arg Gly Lys Thr Leu Val His Ala Glu Ala Gly Asn Ala Lys Gly  
 85 90 95  
 Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly Glu Leu  
 100 105 110  
 Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Asp Thr Ile Lys Lys  
 115 120 125  
 Lys Cys Leu Gly Leu Lys Glu Val Pro Arg Ile Glu Ser Phe His Gly  
 130 135 140  
 Phe Ile Tyr Gly Cys Phe Asp Ala Glu Ala Pro Thr Leu Val Asp Tyr  
 145 150 155 160  
 Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Ile Phe Lys His Ser Gly  
 165 170 175  
 Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys Ala Asn  
 180 185 190  
 Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His Val Gly  
 195 200 205  
 Trp Thr His Ala Ser Ser Leu Arg Ser Gly Gln Ser Ile Phe Thr Pro  
 210 215 220  
 Leu Ala Gly Asn Ala Met Leu Pro Pro Glu Gly Ala Gly Leu Gln Met  
 225 230 235 240

Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly Tyr Ser  
 245 250 255  
 Gly Val His Ser Ala Asp Leu Val Pro Glu Met Met Ala Phe Gly Gly  
 260 265 270  
 Ala Lys Gln Glu Lys Leu Ala Lys Glu Ile Gly Asp Val Arg Ala Arg  
 275 280 285  
 Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn Ser Ile  
 290 295 300  
 Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp Glu Asn  
 305 310 315 320  
 Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met Pro Glu  
 325 330 335  
 Asp Leu Lys Arg Arg Leu Ala Asp Ala Val Gln Arg Thr Val Gly Pro  
 340 345 350  
 Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr Glu Ser  
 355 360 365  
 Gln Asn Ala Lys Lys Tyr Gln Ser Ser Asn Ser Asp Leu Ile Ala Asn  
 370 375 380  
 Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Glu Cys Tyr Pro Gly Val  
 385 390 395 400  
 Val Ala Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe Tyr Arg  
 405 410 415  
 Ala Tyr Gln Ala His Ile Ser Ser Ser Asn Trp Ala Glu Phe Glu Asn  
 420 425 430  
 Thr Ser Arg Asn Trp His Thr Glu Leu Thr Lys Thr Thr Asp Arg  
 435 440 445

&lt;210&gt; 23

&lt;211&gt; 447

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; A polypeptide encoded by SEQ ID NO:12.

&lt;400&gt; 23

Met Ser Tyr Gln Asn Leu Val Ser Glu Ala Gly Leu Thr Gln Lys Leu  
 1 5 10 15  
 Leu Ile His Gly Asp Lys Glu Leu Phe Gln His Glu Leu Lys Thr Ile  
 20 25 30  
 Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile Pro Ser  
 35 40 45  
 Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Val Asp Glu Val Ile Val  
 50 55 60  
 Ser Arg Gln Asn Asp Gly Ser Val Arg Ala Phe Leu Asn Val Cys Arg  
 65 70 75 80  
 His Arg Gly Lys Thr Leu Val His Thr Glu Ala Gly Asn Ala Lys Gly  
 85 90 95  
 Phe Val Cys Gly Tyr His Gly Trp Gly Tyr Gly Ser Asn Gly Glu Leu  
 100 105 110  
 Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Asp Ala Ile Lys Lys  
 115 120 125  
 Lys Cys Leu Gly Leu Lys Glu Val Pro Arg Ile Glu Ser Phe His Gly  
 130 135 140  
 Phe Ile Tyr Gly Cys Phe Asp Ala Glu Ala Pro Pro Leu Ile Asp Tyr  
 145 150 155 160  
 Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Thr Phe Lys His Ser Gly  
 165 170 175  
 Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Val Lys Ala Asn  
 180 185 190  
 Trp Lys Pro Phe Ala Glu Asn Phe Val Gly Asp Ile Tyr His Val Gly  
 195 200 205

Trp Thr His Ala Ala Ala Leu Arg Ala Gly Gln Ser Val Phe Ser Ser  
 210 215 220  
 Leu Ala Gly Asn Ala Lys Leu Pro Pro Glu Gly Ala Gly Leu Gln Met  
 225 230 235 240  
 Thr Ser Lys Tyr Gly Ser Gly Met Gly Leu Thr Trp Asp Tyr Tyr Ser  
 245 250 255  
 Gly Asn Phe Ser Ala Asp Met Val Pro Asp Leu Met Ala Phe Gly Ala  
 260 265 270  
 Ala Lys Gln Glu Lys Leu Ala Lys Glu Ile Gly Asp Val Arg Ala Arg  
 275 280 285  
 Ile Tyr Arg Ser Ile Leu Asn Gly Thr Val Phe Pro Asn Asn Ser Phe  
 290 295 300  
 Leu Thr Gly Ser Ala Thr Phe Lys Val Trp Asn Pro Ile Asp Glu Asn  
 305 310 315 320  
 Thr Thr Glu Val Trp Thr Tyr Ala Phe Val Glu Lys Asp Met Pro Glu  
 325 330 335  
 Asp Leu Lys Arg Arg Leu Ala Asp Ala Ala Gln Arg Ser Val Gly Pro  
 340 345 350  
 Ala Gly Phe Trp Glu Ser Asp Asp Asn Glu Asn Met Glu Thr Leu Ser  
 355 360 365  
 Gln Asn Ala Lys Lys Tyr Gln Ser Ser Asn Ser Asp Gln Ile Ala Ser  
 370 375 380  
 Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Glu Cys Tyr Pro Gly Val  
 385 390 395 400  
 Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe Tyr Arg  
 405 410 415  
 Ala Tyr Gln Ala His Ile Ser Ser Asn Trp Ala Glu Phe Glu Asn  
 420 425 430  
 Ala Ser Arg Asn Trp His Thr Glu Leu Thr Lys Thr Thr Asp Arg  
 435 440 445

<210> 24  
 <211> 451  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> A polypeptide encoded by SEQ ID NO:13.

<400> 24  
 Met Arg Gln Ala Ile Met Ser Tyr Gln Asn Leu Val Ser Glu Ala Gly  
 1 5 10 15  
 Leu Thr Gln Lys His Leu Ile Tyr Gly Asp Lys Glu Leu Phe Gln His  
 20 25 30  
 Glu Leu Lys Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp  
 35 40 45  
 Ser Leu Ile Pro Ser Pro Gly Asp Tyr Val Lys Ala Lys Met Gly Val  
 50 55 60  
 Asp Glu Val Ile Val Ser Arg Gln Asn Asp Gly Ser Val Arg Ala Phe  
 65 70 75 80  
 Leu Asn Val Cys Arg His Arg Gly Lys Thr Ile Val Asp Ala Glu Ala  
 85 90 95  
 Gly Asn Ala Lys Gly Phe Val Cys Gly Tyr His Gly Trp Gly Tyr Gly  
 100 105 110  
 Ser Asn Gly Glu Leu Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly  
 115 120 125  
 Asp Ala Ile Lys Lys Cys Leu Gly Leu Lys Glu Val Pro Arg Ile  
 130 135 140  
 Glu Ser Phe His Gly Phe Ile Tyr Gly Cys Phe Asp Ala Glu Ala Pro  
 145 150 155 160  
 Pro Leu Ile Asp Tyr Leu Gly Asp Val Ala Trp Tyr Leu Glu Pro Thr  
 165 170 175

Phe Lys His Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Ala Lys Val  
     180                 185                 190  
 Val Val Lys Gly Asn Trp Lys Val Phe Ala Glu Asn Phe Val Gly Asp  
     195                 200                 205  
 Ile Tyr His Ile Gly Trp Thr His Ala Ser Ile Leu Arg Ala Gly Gln  
     210                 215                 220  
 Ala Ile Phe Ala Pro Leu Ala Gly Asn Ala Met Leu Pro Pro Glu Gly  
     225                 230                 235                 240  
 Thr Gly Leu Gln Ala Thr Thr Lys Tyr Gly Ser Gly Ile Gly Val Ser  
     245                 250                 255  
 Leu Asp Ala Tyr Ser Gly Val Gln Ser Ala Asp Leu Val Pro Glu Met  
     260                 265                 270  
 Met Ala Phe Gly Gly Ala Lys Gln Glu Lys Leu Ala Lys Glu Ile Gly  
     275                 280                 285  
 Asp Val Arg Ala Arg Ile Tyr Arg Ser Gln Val Asn Gly Thr Val Phe  
     290                 295                 300  
 Pro Asn Asn Cys Phe Leu Thr Gly Ala Gly Val Phe Lys Val Phe Asn  
     305                 310                 315                 320  
 Pro Ile Asp Glu Asn Thr Thr Glu Ala Trp Thr Tyr Ala Ile Val Glu  
     325                 330                 335  
 Lys Asp Met Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ala Ala Gln  
     340                 345                 350  
 Arg Ser Val Gly Pro Ala Gly Tyr Trp Glu Ser Asp Asp Asn Asp Asn  
     355                 360                 365  
 Met Val Leu Ser Gln Asn Ala Lys Lys Tyr Gln Ser Ser Asn Ser Asp  
     370                 375                 380  
 Leu Ile Ala Asp Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Glu Cys  
     385                 390                 395                 400  
 Tyr Pro Gly Val Val Ser Lys Ser Ala Phe Ser Glu Thr Asn His Arg  
     405                 410                 415  
 Gly Phe Tyr Arg Ala Tyr Gln Ala His Ile Ser Ser Ser Asn Trp Ala  
     420                 425                 430  
 Glu Phe Glu Asn Thr Ser Arg Asn Trp His Thr Glu Leu Thr Lys Thr  
     435                 440                 445  
 Thr Asp Arg  
     450

&lt;210&gt; 25

&lt;211&gt; 2265

&lt;212&gt; DNA

&lt;213&gt; Pseudomonas sp.

&lt;400&gt; 25

gagggttagag	aaatcgaatg	cccttgcatt	caaggtcgg	ttgacgttt	cacaggcaaa	60
gccctgtcg	caccgtgc	acagaacatc	aaaacatatac	cagtcaagat	tgagaacctg	120
cgcgtatga	ttgattttag	ctaagaattt	taacaggagg	caccccgggc	cctagagcgt	180
aatcaccccc	attccatctt	ttttaggtga	aaacatgaat	tacaataata	aatcttgg	240
aagtgaatct	ggtctgagcc	aaaagcacct	gattcatggc	gatgaagaac	tttccaaca	300
tgaactgaaa	accatttttgc	cgcggaaactg	gcttttctc	actcatgata	gcctgattcc	360
tgccccccgg	gactatgtt	ccgcaaaaat	ggggattgac	gaggtcatcg	tctcccgca	420
gaacgacgg	tcgattcgt	cttttctgaa	cgtttgcgg	catcgtggca	agacgctgg	480
gagcgtggaa	gccggcaatg	ccaaaggttt	tgtttgcagc	tatcacggct	ggggcttcgg	540
ctccaaacgg	gaaactgcaga	gcgttccatt	tgaaaaagat	ctgtacggcg	agtcgctcaa	600
taaaaaatgt	ctggggttga	aagaagtgc	tcgcgtggag	agttccatg	gcttcatcta	660
cggttgcttc	gaccaggagg	cccctcctt	tatggactat	ctgggtgacg	ctgcttggta	720
cctggAACCT	atgttcaagc	attccggcgg	tttagaactg	gtcggtcctc	caggcaaggt	780
tgtgatcaag	gccaacttgg	aggcacccgc	ggaaaacttt	gtgggagatg	cataaccacgt	840
gggttggacg	cacgcgtctt	cgcttcgctc	gggggagttt	atcttctcg	cgctcgctgg	900
caatgcggcg	ctaccacctg	aaggcgcagg	cttgcggaaatg	acctccaaat	acggcagcgg	960
catgggtgtg	tttgtggacg	gatattcagg	tgtgcatacg	gcagacttgg	ttccggaaatt	1020
gatggcattt	ggaggcgcgg	agcaggaaag	gctgaacaaa	gaaattggcg	atgttcgcgc	1080
tcggatttat	cgcagccacc	tcaactgcac	cgttttcccg	aacaacagca	tgctgacactg	1140

ctcgggtgtt	ttcaaaagtat	ggaacccgat	cgacgcaaac	accaccgagg	tctggaccta	1200
cgcattgtc	aaaaaagaca	tgcctgagga	tctcaagcgc	cgcttggccg	actctgttca	1260
gcgaacgttc	gggcctgctg	gcttctggga	aagcgacgac	aatgacaata	tggaaacagc	1320
ttcgcaaaac	ggcaagaat	atcaatcaag	agatagtat	ctgcttcaa	accttggttt	1380
cggtagggac	gtataccggcg	acgcggctca	tccagggcgtc	gtcggcaat	cgggatcg	1440
c gagaccagt	tatcggtt	tctaccgggc	ttaccaggca	cacgtcagca	gctccaactg	1500
ggctgagttc	gagcatgcct	ctagtacttg	gcatactgaa	cttacgaaga	ctactgtatcg	1560
ctaacagacg	agtgcaccat	gtatcaat	attcaagaag	acaagcttgtt	ttccgcccac	1620
gacgcccgaag	agattttcg	tttcttcaat	tgccacgact	ctgctttgca	acaagaagcc	1680
actacgctgc	tgaccaggaa	agcgcatgg	ttggacatttc	aggcttaccg	tgcttggta	1740
gagcaactg	tggggtcaga	ggtgcaat	caggtcattt	cacgcgaact	gcgcgcagct	1800
tcagagcgtc	gttataaagct	caatgaagcc	atgaacgttt	acaacgaaaa	tttcagcaa	1860
ctgaaaagttc	gagttgagca	tcaactggat	ccgcaaaact	ggggcaacag	cccgaaagctg	1920
cgttttactc	gttttatcac	caacgtccag	gccgcaatgg	acgtaaaatga	caaagagcta	1980
cttcacatcc	gctccaaacgt	cattctgcac	cgggcacgac	gtggcaatca	ggtcgatgtc	2040
ttctacgccc	ccccggaaaga	taaatggaaa	cgtggcgaag	gtggagtacg	aaaattggtc	2100
cagcgattcg	tcgattaccc	agagcgcata	ttcagacgc	acaatctgtat	ggtctttctg	2160
tgattcagtg	accattttta	caaatggtc	ctgcaaccgc	ggtcaccatt	aatcaaaggg	2220
aatgtacgtg	tatggcaat	caacaagtgc	tttcgataac	cggtg		2265

&lt;210&gt; 26

&lt;211&gt; 449

&lt;212&gt; PRT

&lt;213&gt; Pseudomonas sp.

&lt;400&gt; 26

Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln						
1	5	10	15			
Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys						
20	25	30				
Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile						
35	40	45				
Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val						
50	55	60				
Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val						
65	70	75	80			
Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala						
85	90	95				
Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly						
100	105	110				
Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu						
115	120	125				
Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe						
130	135	140				
His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met						
145	150	155	160			
Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His						
165	170	175				
Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys						
180	185	190				
Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His						
195	200	205				
Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe						
210	215	220				
Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu						
225	230	235	240			
Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly						
245	250	255				
Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe						
260	265	270				
Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg						
275	280	285				

Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn  
 290 295 300  
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp  
 305 310 315 320  
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met  
 325 330 335  
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Phe  
 340 345 350  
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr  
 355 360 365  
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu  
 370 375 380  
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro  
 385 390 395 400  
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe  
 405 410 415  
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe  
 420 425 430  
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp  
 435 440 445  
 Arg

<210> 27  
 <211> 2265  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A sequence encoding an NDO mutant.

<400> 27

gagggttagag	aaatcgaatg	ccccttgcat	caaggtcgg	ttgacgtttg	cacaggcaaa	60
gccctgtcg	cacccgtgac	acagaacatc	aaaacatatac	cagtcaagat	tgagaacctg	120
cgcgtatga	ttgattttag	ctaagaattt	taacaggagg	caccccgggc	cctagagcgt	180
aatcaccccc	attccatctt	tttaggtga	aaacatgaat	tacaataata	aatcttggt	240
aagtgaatct	ggtctgagcc	aaaagcacct	gattcatggc	gatgaagaac	ttttccaaca	300
tgaactgaa	accattttt	cgcggaaactg	gcttttctc	actcatgata	gcctgattcc	360
tgcccccggc	gactatgtt	ccgaaaaat	ggggattgac	gaggtcatcg	tctccggca	420
gaacgacgg	tcgattcgt	ctttctgaa	cgtttgcgg	catcgtggca	agacgctgg	480
gagcgtggaa	gccggcaatg	ccaaagg	ttttgcagc	tatcacggct	ggggcttcgg	540
ctccaacgg	gaactgcaga	gcgttccatt	tgaaaaagat	ctgtacggcg	agtcgctcaa	600
taaaaaatgt	ctgggggtt	agaagtcgc	tcgcgtggag	agttccatg	gttccatcta	660
cggtgcttc	gaccaggagg	cccctctt	tatggactat	ctgggtgacg	ctgcttgta	720
cctggAACCT	atgttcaagc	attccgggg	tttagaactg	gtcggtcctc	caggcaaggt	780
tgtgatcaag	gccaactgga	aggcacccgc	ggaaaaacttt	gtgggagatg	cataccacgt	840
gggttggacg	cacgcgtctt	cgcttcgctc	gggggagtct	atcttctgt	cgctcgctgg	900
caatgcggcg	ctaccacctg	aaggcgcagg	cttgc	acccatcgat	acggcagcgg	960
catgggtgt	ttgtgggacg	gatattcagg	tgtgcata	gcagacttgg	ttccggaaatt	1020
gatggcattc	ggaggcgcaa	agcaggaaag	gctgaacaaa	gaaattggcg	atgttcgcgc	1080
tcggatttat	cgcagccacc	tcaactgcac	cgtttcccg	aacaacagca	tgctgacctg	1140
ctcgggtgtt	ttcaaaagtat	ggaacccgat	cgacgc	accacccgagg	tctggaccta	1200
cggcattgtc	gaaaaagaca	tgcctgagga	tctcaagcgc	cgcttggccg	actctgttca	1260
gcaacgggc	gggcctgctg	gcttctggga	aagcgc	aatgacaata	tggaaacagc	1320
ttcgcaaaac	ggcaagaaat	atcaatcaag	agatagtat	ctgtttcaa	accttgggtt	1380
cggtgaggac	gtatacggcg	acgcggtcta	tccaggcg	gtcggcaat	cggcgatcgg	1440
cgagaccagt	tatcg	tctaccgggc	ttaccaggca	cacgtcagca	gctccaactg	1500
ggctgagttc	gagcatgcct	ctagactt	gcatactgaa	cttacgaaga	ctactgatcg	1560
ctaacagacg	agtcgaccat	gatgatcaat	attcaagaag	acaagctgtt	ttccgcccac	1620
gacgcccgaag	agattttcg	tttcttcaat	tgccacgact	ctgcttgc	acaagaagcc	1680
actacgctgc	tgacc	cagg	aggcttaccg	tgcttgg	tgcttggta	1740
gagcactgcg	tggggtcaga	ggtgcaat	caggcattt	cacgcgact	gcgcgcagct	1800

tcagagcgto	gttataagct	caatgaagcc	atgaacgaaa	acaacgaaaa	ttttcagcaa	1860
ctgaaagtto	gagttgagca	tcaactggat	ccgcaaaaact	ggggcaacag	cccgaagctg	1920
cgtttactc	gctttatcac	caacgtccag	gccgcaatgg	acgtaaaatga	caaagagcta	1980
cttcacatcc	gctccaaacgt	cattctgcac	cgggcacgac	gtggcaatca	ggtcgatgtc	2040
tttacgccc	ccccggaaaga	taaatggaaa	cgtggcgaag	gtggagtacg	aaaattggtc	2100
cagcgattcg	tcgattaccc	agagcgcata	cttcagacgc	acaatctgtat	ggtctttctg	2160
tgattcagtg	accattttta	caaatggtc	ctgcaaccgc	ggtcaccatt	aatcaaagg	2220
aatgtacgtg	tatggcaat	caacaagtgc	tttcgataac	cggtg		2265

&lt;210&gt; 28

&lt;211&gt; 2265

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; A sequence encoding an NDO mutant.

&lt;400&gt; 28

gagggtagag	aaatcgaaatg	ccccttgcat	caaggtcgg	ttgacgtttgc	cacaggcaaa	60
gcctgtcg	caccctgtac	acagaacatc	aaaacatatc	cagtcaagat	tgagaacctg	120
cgcgtatgc	ttgatttgc	ctaagaattt	taacaggagg	cacccgggc	cctagagcgt	180
aatcaccatcc	attccatctt	ttttaggtga	aaacatgaat	tacaataata	aaatcttgg	240
aagtgaatct	ggtctgagcc	aaaagcacct	gattcatggc	gttgaagaac	ttttccaaca	300
tgaactgaaa	accatttttgc	cgcggactgc	gtttttctc	actcatgata	gcctgattcc	360
tgccccccgc	gactatgttgc	ccgcaaaaat	ggggatttgc	gaggtcate	tctccggca	420
gaacgacgg	tcgatttgc	ctttctgaa	cgtttgcgg	catcggtgg	agacgcttgt	480
gagcgtggaa	gccggcaatg	ccaaagggtt	tgtttgcgc	tatcaggcg	ggggcttcgg	540
ctccaacgg	gaactgcaga	ggttccatt	tgaaaaaagat	ctgtacggcg	agtcgctcaa	600
taaaaaatgt	ctgggggttgc	aagaagtcgc	tcgcgtggag	agttccat	gttcatcta	660
cggttgttgc	gaccaggagg	cccttctct	tatggactat	ctgggtgc	ctgttggta	720
ccttggaaac	atgttcaagc	atccggcg	tttagaactgc	gtcggtctc	caggcaaggt	780
tgtatcaag	gccaactgga	aggcaccggc	ggaaaaacttt	gtgggagatg	cataaccacgt	840
gggttggacg	cacgcgttgc	cggttcgtc	ggggggagtct	acttctcg	cgctcgctgg	900
caatgcggcg	ctaccacgt	aggcgcagg	tttgc	acccat	acggcagcgg	960
catgggtgt	tttggggacg	gatattcagg	tgtgcata	gcagacttgg	ttccggaaatt	1020
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tcggatttat	cgccggcacc	tcaactgcac	cggttcccg	aacaacagca	tgctgacctg	1140
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actacgctgc	tgaccccg	aggcatttgc	tttgc	aggcttac	tgcttgg	1740
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tcagagcg	gttataagct	caatgaagcc	atgaacgaaa	acaacgaaaa	ttttcagca	1860
ctgaaagtgc	gagttgagca	tcaactggat	ccgcaaaaact	ggggcaacag	cccgaagctg	1920
cgtttactc	gctttatcac	caacgtccag	gccgcaatgg	acgtaaaatga	caaagagcta	1980
cttcacatcc	gctccaaacgt	cattctgcac	cgggcacgac	gtggcaatca	ggtcgatgtc	2040
tttacgccc	ccccggaaaga	taaatggaaa	cgtggcgaag	gtggagtac	aaaattgg	2100
cagcgattcg	tcgattaccc	agagcgcata	cttcagacgc	acaatctgtat	ggtctttctg	2160
tgattcagtg	accattttta	caaatggtc	ctgcaaccgc	ggtcaccatt	aatcaaagg	2220
aatgtacgtg	tatggcaat	caacaagtgc	tttcgataac	cggtg		2265

&lt;210&gt; 29

&lt;211&gt; 2265

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; A sequence encoding an NDO mutant.

&lt;400&gt; 29

gagggttagag	aaatcgaaatg	ccccttgc	caaggtcgg	ttgacgttg	cacaggcaaa	60
gccctgtgcg	caccctgtac	acagaacatc	aaaacat	cagtcaagat	tgagaacctg	120
cgcgtaatga	ttgatttgag	ctaagaattt	taacaggagg	caccccg	cctagagcgt	180
aatcacc	attccatctt	ttttaggtga	aaacatgaat	tacaataata	aaatcttgg	240
aagtgaatct	ggtctgagcc	aaaagcacot	gattcatggc	gatgaagaac	ttttccaaca	300
tgaactgaaa	accatttttgc	cgcggaaactg	gcttttctc	actcatgata	gcctgattcc	360
tgccccccggc	gactatgtta	cgcacaaaat	ggggattgac	gaggtcatcg	tctccggca	420
gaacgacggt	tcgattcgtg	ctttctgaa	cgtttgcgg	catcg	agacgctgg	480
gagcgtggaa	gccggcaatg	coaaagg	ttttgcagc	tatcacgg	ggggcttcgg	540
ctccaacgggt	gaactgcaga	gcttccatt	tgaaaaagat	ctgtacggcg	agtcgctcaa	600
taaaaaatgt	ctgggggtga	aagaagtgc	tcgcgtggag	agcttccatg	gttcatcta	660
cgttgc	gaccaggagg	cccctcctct	tatggactat	ctgggtgacg	ctgcttggta	720
cctggaacct	atgttcaagc	atccggcg	tttagaactg	gtcggtcc	caggcaaggt	780
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caatgcggcg	ctaccac	ctg	aaaggcgcagg	cttgc	acccgcgg	960
catgggtgt	ttgtggacg	gatattcagg	tgtgcata	gcagacttgg	ttccggaaatt	1020
gatggcattc	ggaggcg	agcaggaaag	gctgaa	gaaattggcg	atgttcgc	1080
tcgatttat	cgcagccacc	tcaactgc	cgtttcc	aacaacagc	tgctgac	1140
ctcggtgtt	ttcaagat	ggaacccgat	cgacgc	accacgg	tctggac	1200
cgccattgtc	gaaaaagaca	tgc	tctcaagc	cgcttgg	actctgttca	1260
gcaacgacc	gggcctgt	gcttctgg	aagcgac	aatgacaata	tggaaacagc	1320
ttcgaaaac	ggcaagaat	atcaatca	agatagt	ctgtttc	accttgg	1380
cgg	gtatacggc	acgcgt	tccaggc	gtcg	cggc	1440
cgagaccagt	tatcg	tttacccgg	ttaccagg	cacgtc	acttcaact	1500
ggctgagttc	gagcatgc	ctagactt	gcata	tttac	ctactgat	1560
ctaacagacg	agtgc	gatgatca	attcaaga	acaagct	ttccccc	1620
gacgccc	agatttctc	tgcc	tgccacg	ctgcttgc	acaaga	1680
actacgctgc	tgaccc	aggcattt	ttggacat	aggcttac	tgcttgg	1740
gagca	tggggtc	ggtc	cagg	cacgc	gcgc	1800
tca	gttataag	caatgaa	atgaa	acaacg	ttttc	1860
ctgaaagttc	gat	tcactggat	ccgcaaa	ggggca	cccga	1920
cgttta	actc	caacgtcc	ggc	acgt	aaagagct	1980
cttcacatcc	gttcc	ac	ccgc	aaat	caaa	2040
tttac	ccgg	aaaatgg	cg	gg	tttgc	2100
cagcgattcg	tcg	attaccc	agagc	cata	tttgc	2160
tgattc	acc	tttcaaaatgg	ctg	caacc	tttgc	2220
aatgtacgtg	tat	ggcaat	caaca	ggc	tttgc	2265

&lt;210&gt; 30

&lt;211&gt; 2265

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; A sequence encoding an NDO mutant.

&lt;400&gt; 30

gagggttagag	aaatcgaaatg	ccccttgc	caagg	ttgacgtt	cacaggcaaa	60
gccctgtgcg	caccctgtac	acagaacatc	aaaacat	cagtcaagat	tgagaacctg	120
cgcgtaatga	ttgatttgag	ctaagaattt	taacaggagg	caccccg	cctagagcgt	180
aatcacc	attccatctt	ttttaggtga	aaacatgaat	tacaataata	aaatcttgg	240
aagtgaatct	ggtctgagcc	aaaagcacot	gattcatggc	gatgaagaac	ttttccaaca	300
tgaactgaaa	accattttgc	cgcggaaactg	gcttttctc	actcatgata	gcctgattcc	360
tgccccccggc	gactatgtta	cgcacaaaat	ggggattgac	gaggtcatcg	tctccggca	420
gaacgacggt	tcgattcgtg	ctttctgaa	cgtttgcgg	catcg	agacgctgg	480
gagcgtggaa	gccggcaatg	coaaagg	ttttgcagc	tatcacgg	ggggcttcgg	540
ctccaacgggt	gaactgcaga	gcgttcc	tgaaaaagat	ctgtacggcg	agtcgctcaa	600

taaaaatgt	ctggggttga	aagaagtcgc	tcgcgtggag	agcttccatg	gcttcatacta
cgttgcctc	gaccaggagg	cccctccctt	tatggactat	ctgggtgacg	ctgcttggta
cctggAACCT	atgttcaagc	attccggcgg	tttagaactg	gtcggtcctc	caggcaaggt
tgtgatcaag	gccaacttgg	aggcacccgc	ggaaaacttt	gtgggagatg	cataaccacgt
gggttggacg	cacgcgtctt	cgcttcgctc	ggggggagttct	atcttctcg	cgctcgctgg
caatgcggcg	ctaccacactg	aaggcgcagg	ottgcaaatt	acctccaaat	acggcagcgg
catgggtgtg	tttgtgggacg	gatattcagg	tgtgcatacg	gcagacttgg	ttccggaaatt
gatggcattc	ggaggcgcaa	agcagggaaag	gctgaacaaa	gaaattggcg	atgttgcgc
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gcoaagcctc	gggcctgctg	gcttcggg	aagcgc当地	aatgacaata	tggaaacacg
ttcgaaaac	ggcaagaaaat	atcaatcaag	agatagtgtat	ctgccttcaa	accttggg
cggtgaggac	gtatacggcg	acgcggctta	tccaggcg	gtcgcaaat	cggcgatcgg
cgagaccagt	tatcgtgggt	tctaccggc	ttaccaggca	cacgtcagca	gctccaactg
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cgctttactc	gttattatcac	caacgtccag	gccgcaatgg	acgtaaatga	caaagagcta
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ttctacgccc	cccgaaaaga	taaatggaaa	cgtggc当地	gtggagatcg	aaaattggtc
cagcgattcg	tcgatttaccc	agagcgcata	cttcagacgc	acaatctgtat	ggtcttctg
tgattcagtg	accatttta	caaatggca	ctgcaaccgc	ggtc当地	aatcaaagg
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<210> 31
<211> 2265
<212> DNA
<213> Artificial Sequence
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<220>  
<223> A sequence encoding an NDO mutant.

<400> 31	gagggttagag	aatcgaatg	ccccttgcat	caaggtcgg	ttgacgttt	cacaggcaaa	60
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cgcgtaatga	ttgattttag	ctaagaattt	taacaggagg	caccccgggc	cctagagcgt	180	
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aagtgaatct	ggtctgagcc	aaaagcacct	gattcatggc	gatgaagaac	tttccaaca	300	
tgaactgaaa	accattttg	cgcggaaactg	gcttttctc	actcatgata	gcctgattcc	360	
tgc(ccccggc)	gactatgtt	ccgaaaaat	ggggattgac	gaggtcatcg	tctccggca	420	
gaacgacggt	tcgattcg	cttttctgaa	cggttgcgg	catcgtggca	agacgctggt	480	
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cctggAACCT	atgttcaagg	atccccgg	tttagaactg	gtcggtcctc	caggcaaggt	780	
tgtgatcaag	gccaactgga	aggcacccgc	ggaaaactt	gtgggagatg	cataaccacgt	840	
gggttggacg	cacgcgtt	cgcttcgc	gggggagatct	atcttctcg	cgctcgctgg	900	
caatgcggcg	ctaccac	aaggcgcagg	ttgcaatg	acctccaaat	acggcagcgg	960	
catgggtgt	ttgtgggac	gatattcagg	tgtgcata	gcagacttgg	ttccggaaatt	1020	
gatggcattc	ggaggcgc	agcagggaa	gctgaacaaa	gaaattggcg	atgttgcgc	1080	
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ttcgaaaac	ggcaagaaat	atcaatcaag	agatagtgtat	ctgcttcaa	accttgg	1380	
cggtgaggac	gtatacggcg	acgcggct	tccaggcg	gtcgcaat	cgcgatcg	1440	

cgagaccagt tatacggtt ttaccgggc ttaccaggca cacgtcagca gctccaactg	1500
ggctgagttc gagcatgcct ctagtacttg gcatactgaa cttacgaaga ctactgatcg	1560
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cagcgattcg tgcattaccc agagcgcata cttcagacgc acaatctgtat ggtcttctg	2160
tgattcagtg accattttt caaatggtca ctgcaaccgc ggtcaccatt aatcaaaggg	2220
aatgtacgtg tatggcaat caacaagtgc ttgcataac cggtg	2265

&lt;210&gt; 32

&lt;211&gt; 449

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; A polypeptide encoded by SEQ ID NO:27.

&lt;400&gt; 32

Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln	
1 5 10 15	
Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys	
20 25 30	
Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile	
35 40 45	
Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val	
50 55 60	
Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val	
65 70 75 80	
Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala	
85 90 95	
Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly	
100 105 110	
Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu	
115 120 125	
Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe	
130 135 140	
His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met	
145 150 155 160	
Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His	
165 170 175	
Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys	
180 185 190	
Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His	
195 200 205	
Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe	
210 215 220	
Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu	
225 230 235 240	
Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly	
245 250 255	
Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe	
260 265 270	
Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg	
275 280 285	
Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn	
290 295 300	

Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp  
 305 310 315 320  
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met  
 325 330 335  
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Gly  
 340 345 350  
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr  
 355 360 365  
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu  
 370 375 380  
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro  
 385 390 395 400  
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe  
 405 410 415  
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Asn Trp Ala Glu Phe  
 420 425 430  
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp  
 435 440 445  
**Arg**

<210> 33  
 <211> 449  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> A polypeptide encoded by SEQ ID NO:28.

<400> 33  
 Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln  
 1 5 10 15  
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys  
 20 25 30  
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile  
 35 40 45  
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val  
 50 55 60  
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val  
 65 70 75 80  
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala  
 85 90 95  
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly  
 100 105 110  
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu  
 115 120 125  
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe  
 130 135 140  
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met  
 145 150 155 160  
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His  
 165 170 175  
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys  
 180 185 190  
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His  
 195 200 205  
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe  
 210 215 220  
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu  
 225 230 235 240  
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly  
 245 250 255

Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe  
     260                 265                 270  
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg  
     275                 280                 285  
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn  
     290                 295                 300  
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp  
     305                 310                 315                 320  
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met  
     325                 330                 335  
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Ala  
     340                 345                 350  
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr  
     355                 360                 365  
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu  
     370                 375                 380  
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro  
     385                 390                 395                 400  
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe  
     405                 410                 415  
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe  
     420                 425                 430  
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp  
     435                 440                 445  
 Arg

<210> 34  
 <211> 449  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> A polypeptide encoded by SEQ ID NO:29.

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 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys  
     20                 25                 30  
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile  
     35                 40                 45  
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val  
     50                 55                 60  
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val  
     65                 70                 75                 80  
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala  
     85                 90                 95  
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly  
     100                 105                 110  
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu  
     115                 120                 125  
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe  
     130                 135                 140  
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met  
     145                 150                 155                 160  
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His  
     165                 170                 175  
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys  
     180                 185                 190  
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His  
     195                 200                 205

Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe  
 210 215 220  
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu  
 225 230 235 240  
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly  
 245 250 255  
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe  
 260 265 270  
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg  
 275 280 285  
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn  
 290 295 300  
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp  
 305 310 315 320  
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met  
 325 330 335  
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Thr  
 340 345 350  
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr  
 355 360 365  
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu  
 370 375 380  
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro  
 385 390 395 400  
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe  
 405 410 415  
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe  
 420 425 430  
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp  
 435 440 445  
 Arg

<210> 35  
 <211> 449  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> A polypeptide encoded by SEQ ID NO:30.

<400> 35  
 Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln  
 1 5 10 15  
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys  
 20 25 30  
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile  
 35 40 45  
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val  
 50 55 60  
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val  
 65 70 75 80  
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala  
 85 90 95  
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly  
 100 105 110  
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu  
 115 120 125  
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe  
 130 135 140  
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met  
 145 150 155 160

Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His  
                   165                 170                 175  
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys  
                   180                 185                 190  
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His  
                   195                 200                 205  
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe  
                   210                 215                 220  
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu  
                   225                 230                 235                 240  
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly  
                   245                 250                 255  
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe  
                   260                 265                 270  
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg  
                   275                 280                 285  
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn  
                   290                 295                 300  
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp  
                   305                 310                 315                 320  
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met  
                   325                 330                 335  
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Leu  
                   340                 345                 350  
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr  
                   355                 360                 365  
 Ala Ser Gln Asn Gly Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu  
                   370                 375                 380  
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro  
                   385                 390                 395                 400  
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe  
                   405                 410                 415  
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe  
                   420                 425                 430  
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp  
                   435                 440                 445  
 Arg

<210> 36  
 <211> 449  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> A polypeptide encoded by SEQ ID NO:31.

<400> 36  
 Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln  
     1              5                 10                 15  
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys  
     20             25                 30  
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile  
     35             40                 45  
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val  
     50             55                 60  
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val  
     65             70                 75                 80  
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala  
     85             90                 95  
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly  
     100            105                 110

Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu  
     115                     120                     125  
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe  
     130                     135                     140  
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met  
     145                     150                     155                     160  
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His  
     165                     170                     175  
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys  
     180                     185                     190  
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His  
     195                     200                     205  
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe  
     210                     215                     220  
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu  
     225                     230                     235                     240  
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly  
     245                     250                     255  
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe  
     260                     265                     270  
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg  
     275                     280                     285  
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn  
     290                     295                     300  
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp  
     305                     310                     315                     320  
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met  
     325                     330                     335  
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Ile  
     340                     345                     350  
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr  
     355                     360                     365  
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu  
     370                     375                     380  
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro  
     385                     390                     395                     400  
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe  
     405                     410                     415  
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe  
     420                     425                     430  
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp  
     435                     440                     445  
 Arg

<210> 37  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A mutagenic oligonucleotide.

<400> 37  
 ttcagcgaac ggtcgggcct gc

<210> 38  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> A tetracycline repair oligonucleotide.

<400> 38

gccgggcctc ttgcggata tcgtcca

27

<210> 39

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> An ampicillin knockout oligonucleotide.

<400> 39

gttgccattg ctgcaggcat cgtggtg

27

<210> 40

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> A mutagenic oligonucleotide.

<400> 40

gaggcacccg cggaagcttt tgtgggagat gca

33

<210> 41

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> A mutagenic oligonucleotide.

<400> 41

gcaccccgcg aacaatttgtt gggagatgca

30

<210> 42

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> A mutagenic oligonucleotide.

<400> 42

ccgcggaaag ctttgtggga g

21

<210> 43

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> A mutagenic oligonucleotide.

<400> 43

ccgcggaaaa gcttgtggga gatg

24

<210> 44

<211> 23

<212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A mutagenic oligonucleotide.

<400> 44  
 cgccggaaaaac gttgtgggag atg 23

<210> 45  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A mutagenic oligonucleotide.

<400> 45  
 atattcaggt gcgcatacg cag 23

<210> 46  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A mutagenic oligonucleotide.

<400> 46  
 ggacggatat tcagggctcc atagcgcaga cttg 34

<210> 47  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A mutagenic oligonucleotide.

<400> 47  
 gacggatatt caggtAACCA tagcgcAGAC ttg 33

<210> 48  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A mutagenic oligonucleotide.

<400> 48  
 ggtgtttca aagtCGCgaa cccgatcgac 30

<210> 49  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A mutagenic oligonucleotide.

<400> 49

ctgttcagcg aaacttcggg cctgct	26
<210> 50	
<211> 26	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> A mutagenic oligonucleotide.	
<400> 50	
ctgttcagcg aaggttcggg cctgct	26
<210> 51	
<211> 26	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> A mutagenic oligonucleotide.	
<400> 51	
ctgttcagcg aagcttcggg cctgct	26
<210> 52	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> A mutagenic oligonucleotide.	
<400> 52	
ttcagcgaac gctcgggcct gc	22
<210> 53	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> A mutagenic oligonucleotide.	
<400> 53	
ggcctgctgg ct当地cggaa agcgacgaca	30
<210> 54	
<211> 21	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> A mutagenic oligonucleotide.	
<400> 54	
gaaagcgcacg ccaatgacaa t	21
<210> 55	
<211> 30	
<212> DNA	
<213> Artificial Sequence	

&lt;220&gt;

&lt;223&gt; A mutagenic oligonucleotide.

&lt;400&gt; 55

acgacaatga caattggaa acagcttcgc

30

&lt;210&gt; 56

&lt;211&gt; 2265

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; A sequence encoding an NDO mutant.

&lt;400&gt; 56

gaggtagag aaatcgaatg ccccttgcat	caaggcggt ttgacgtttgcacaggcaaa	60
gccctgtgcg caccgtgac acagaacatc	aaaacatatc cagtcaagat tgagaacctg	120
cgcgtaatga ttgattttag	ctaagaattt taacaggagg caccggc cctagagcgt	180
aatcaccccc attccatctt	ttttaggtga aaacatgaat tacaataata aaatcttgg	240
aagtgaatct ggtctgagcc	aaaaggcacct gattcatggc gatgaagaac tttccaaca	300
tgaactgaaa accatttttgcg	cgccgaaactg gcttttctc actcatgata gcctgattcc	360
tgcccccggc gactatgtt	ccgcaaaaat ggggattgac gaggtcatcg tctccggca	420
gaacgacggt tcgattctgt	cttttctgaa cgtttgcgg catcggtggca agacgctgg	480
gagcgtggaa gccggcaatg	ccaaagggtt tgtttgcggc tacacggct gggcttccgg	540
ctccaaacgggt	gaactgcaga gctgttccatt tgaaaaagat ctgtacggcg agtcgctcaa	600
taaaaaatgt ctgggttga	aagaagtgc tcgcgtggag agcttccatg gcttcatcta	660
cgggtgttcc gaccaggagg	cccttcctct tatgactat ctgggtgacg ctgttggta	720
cctggAACCT atgttcaagc	attccggggggtttagaactgt gtcggtcctc caggcaagg	780
tgtgatcaag gccaacttgg	aggcaccggc ggaaaaactttt gtgggagatg cataccacgt	840
gggttggacg cacgcgttcc	cgcttcgtc gggggagtct atcttctcg tgcgtcgctgg	900
caatcgccgc	ctaccacctg aaggcgcagg cttgcaatgc acctccaaat acggcagcgg	960
catgggtgtg ttgtggacg	gatattcagg tgtgcatagc gcagacttgg ttcggaaatt	1020
gatggcatttgcg	ggaggcgcaaa agcaggaaag gctgaacaaa gaaattggcg atgttgcgc	1080
tcggatttatcg	cgcagccacc tcaactgcac cggtttcccg aacaacagca tgctgacctg	1140
ctcgggtgtt ttcaaaatgt	ggaacccgat cgacgcacaaac accacggagg tctggaccta	1200
cgccattgtc	gaaaaagaca tgcctgagga tctcaagcgc cgcttggccg actctgttca	1260
gccaacgtgg	gggcctgtcg gttctggaa aagcgcacgc aatgacaataa tgaaaacagc	1320
ttcgcaaaac	ggcaagaaat atcaatcaag agatagtgtat ctgttttcaa accttgggtt	1380
cggtgaggac	gtatacggcg acgcggctta tccaggcg tcggcaaat cggcgatcg	1440
cgagacgtt	tatcggtgtt tctaccggggc ttaccaggca cacgtcagca gcttcaactg	1500
ggctgagttc	gagcatgcct ctatgtacttgc gataactgaa cttacgaaga ctactgtcg	1560
ctaacagacg	agtcgaccat gatgatcaat attcaagaag acaagctgtt ttcggccac	1620
gacgcccgaag	agattttcg tttcttcaat tgccacgact ctgttttgc acaagaagcc	1680
actacgtgc	tgaccggaga agcgcatttgc ttggacattc aggettacgg tgcttggta	1740
gagcactcg	tggggtcaga ggtgaatattt caggtcattt cacgcgaact gcgcgcagct	1800
tcagagcg	tttataaactt caatgaagcc atgaacgttt acaacgaaaaa tttcagcaa	1860
ctgaaaatgt	gagttgagca tcaactggat ccgcacaaact gggcaacag cccgaagctg	1920
cgtttactc	gttttactc caacgtccag gcccgaatgg acgtaaatga caaagagcta	1980
cttcacatcc	gttccaaacgt cattctgcac cgggcacgac gtggcaatca ggtcgatgtc	2040
ttctacgccc	ccccggaaataa atatggaaa cgtggcgaaat gtggagtacg aaaattggtc	2100
cagcgattcg	tcgatttaccc agagcgcata cttcagacgc acaatctgtat ggttttctg	2160
tgattcagt	accatttttcaaaatgtca ctgcaaccgc ggtcaccatt aatcaaagg	2220
aatgtacgt	tatggcaat caacaaggcg ttgcataac cggtg	2265

&lt;210&gt; 57

&lt;211&gt; 2265

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; A sequence encoding an NDO mutant.

<400> 57

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gagggttagag aaatcaaatg ccccttgcatt caaggctgg tttacgtttt cacaggcaaa      60
gccctgtcgcc accccgtgac acagaacatc aaaacatatac cagtcaagat tgagaacctg    120
cgcgtaatga ttgatttgag ctaagaattt taacaggagg caccggcgc cctagagcgt    180
aatcaccccc attccatctt ttttaggtga aaacatgaat tacaataata aaatcttggt    240
aagtgaatct ggtctgagcc aaaaggcacct gattcatggc gatgaagaac ttttccaaca    300
tgaactgaaa accattttg cgccggactg gcttttctc actcatgata gcctgattcc    360
tgccccggc gactatgtta ccgcaaaaat ggggattgac gaggtcatcg tctccggca    420
gaacgacggc tcgattctgt ctttctgaa cggttgcgg catcggtggca agacgctggt    480
gagcgtggaa gcccggcaatg ccaaagggttt tggttgcagc tatcacggct ggggcttcgg    540
ctccaacggc gaactgcaga gctgtccatt tgaaaaagat ctgtacggcg agtcgctaa    600
taaaaaatgt ctgggggttga aagaagtcgc tcgcgtggag agttccatg gcttcatcta    660
cggttgcctc gaccaggagg cccctctct tatggactat ctgggtgacg ctgttggta    720
ccttggaaacct atgttcaagg atccggcgg tttagaactg gtcggccctc caggcaaggt    780
tgtgatcaag gccaacttggaa aggcccccggc ggaaaaacttt gtgggagatg cataaccacgt    840
gggttggacg cacgcgtt cgttcgtctc gggggagtct atttctctg cgctcgctgg    900
caatgcggcg ctacccatcg aaggcgcagg cttgcaaatg acctccaaat acggcagcgg    960
catgggtgtg ttgtgggacg gatattcagg tgcgtatagc gcagacttgg ttccggaaatt   1020
gatggcattt ggaggcgcggc aagcaggaaag gctgaacaaa gaaattggcg atgttcgcgc   1080
tcggatttat cgcagccacc tcaactgcac cggttcccg aacaacagca tgctgacctg   1140
ctcggtgtt ttcaaaatgt ggaacccgtat cgacgcggc accaccggagg tctggaccta   1200
cgccattgtc gaaaaagaca tgcctgagga tctcaagcgc cgcttggccg actctgttca   1260
gcaacggcggc gggcctgctg gttctggga aagcgcacgac aatgacaata tgaaaacagc   1320
ttcgcaaaac ggcagaataat atcaatcaag agatagtgtat ctgcttcaa accttggttt   1380
cggtgaggac gtatacggcg acgcggctca tccaggcgtc gtcggcaaat cggcgatcgg   1440
cgagaccagt ttcgtgtt tetaccgggc ttaccaggca cacgtcagca gctccaactg   1500
ggctgagttc gacgtgcct ctgtacttg gcatactgaa cttacgaaga ctactgtcg   1560
ctaacagacg agtcgaccat gatgtcaat attcaagaag acaagctggt ttccgcccac   1620
gacgcggaaag agattttcg tttcttcaat tgccacgact ctgcttgc acaagaagcc   1680
actacgctgc tgacccaggaa agcgcatttgg tggacattt aggcttaccg tgcttggta   1740
gagcaactgcg tggggtcaga ggtcaatat caggtcattt cacgcgaact ggcgcgcagct   1800
tcagagcgtc gttataagct caatgaagcc atgaacgttt acaacgaaaaa tttttagca   1860
ctgaaagttc gagttgagca tcaactggat ccgcggaaact ggggcaacag cccgaagctg   1920
cggtttactc gtttatcac caacgtccag gcccgaatgg acgtaaatga caaagagcta   1980
cttcacatcc gtcacatcg cattctgcac cgggcacgac gtggcaatca ggtcgtatgtc   2040
ttctacggcc cccggaaaga taaatggaaa cgtggcgaag gtggagtagc aaaattggtc   2100
cagcgttccg tcgattaccc agagcgcata cttcagacgc acaatctgtat ggtcttctg   2160
tgattcagtg accatttttcaaaatgtca ctgcaaccgc ggtcaccatt aatcaaaggg   2220
aatgtacgtg tatggcaat caacaagtcg tttcgataac cggtg   2265

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&lt;210&gt; 58

&lt;211&gt; 449

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; A polypeptide encoded by SEQ ID NO:56.

&lt;400&gt; 58

Met	Asn	Tyr	Asn	Asn	Lys	Ile	Leu	Val	Ser	Glu	Ser	Gly	Leu	Ser	Gln
1						5			10				15		
Lys	His	Leu	Ile	His	Gly	Asp	Glu	Glu	Leu	Phe	Gln	His	Glu	Leu	Lys
									20	25			30		
Thr	Ile	Phe	Ala	Arg	Asn	Trp	Leu	Phe	Leu	Thr	His	Asp	Ser	Leu	Ile
									35	40			45		
Pro	Ala	Pro	Gly	Asp	Tyr	Val	Thr	Ala	Lys	Met	Gly	Ile	Asp	Glu	Val
									50	55			60		
Ile	Val	Ser	Arg	Gln	Asn	Asp	Gly	Ser	Ile	Arg	Ala	Phe	Leu	Asn	Val
									65	70			75		80
Cys	Arg	His	Arg	Gly	Lys	Thr	Leu	Val	Ser	Val	Glu	Ala	Gly	Asn	Ala
									85	90			95		

Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly  
     100                 105                 110  
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu  
     115                 120                 125  
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe  
     130                 135                 140  
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met  
     145                 150                 155                 160  
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His  
     165                 170                 175  
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys  
     180                 185                 190  
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His  
     195                 200                 205  
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe  
     210                 215                 220  
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu  
     225                 230                 235                 240  
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly  
     245                 250                 255  
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe  
     260                 265                 270  
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg  
     275                 280                 285  
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn  
     290                 295                 300  
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp  
     305                 310                 315                 320  
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met  
     325                 330                 335  
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Trp  
     340                 345                 350  
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr  
     355                 360                 365  
 Ala Ser Gln Asn Gly Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu  
     370                 375                 380  
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro  
     385                 390                 395                 400  
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe  
     405                 410                 415  
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe  
     420                 425                 430  
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp  
     435                 440                 445  
 Arg

<210> 59  
 <211> 449  
 <212> PRT  
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 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu  
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 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe  
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 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg  
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 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn  
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 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp  
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 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met  
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 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Tyr  
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 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr  
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 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu  
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 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro  
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 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe  
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